

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffrey E. Russell Examiner #: 62785 Date: 2-3-2005Art Unit: 1654 Phone Number 3571-272-0769 Serial Number: 101001945Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle) PAPER DISK E-MAIL
REM 3C18 (mailbox), 3D19 (office)

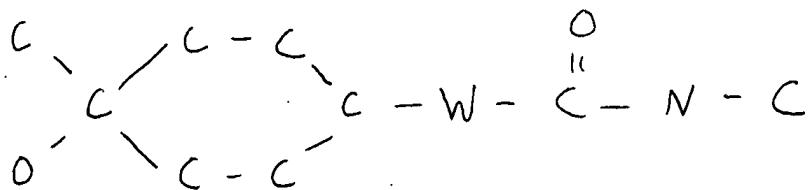
If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Modulation Of AngiogenesisInventors (please provide full names): G.Olson, C.Self, L.Lee, C.Cook, J.Birktaft, B.Morgan,
C.Arico-MuendelEarliest Priority Filing Date: 11-1-2001

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search the following partial structure:



where W is O or N.

Thank you.

JER

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 12:15:42 ; Search time 163 Seconds
(without alignments)
16.609 Million cell updates/sec

Title: US-10-001-945A-16

Perfect score: 26

Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1171057

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

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| 2 | 26 | 100.0 | 7 | 5 | AAE26707 | | Aae26707 Matrix me |
| 3 | 26 | 100.0 | 7 | 7 | ADC33666 | | Adc33666 Matrix me |
| 4 | 26 | 100.0 | 7 | 7 | ADC33667 | | Adc33667 Matrix me |
| 5 | 26 | 100.0 | 7 | 7 | AAE39186 | | Aae39186 Angiogene |
| 6 | 26 | 100.0 | 7 | 7 | AAE39185 | | Aae39185 Angiogene |
| 7 | 26 | 100.0 | 7 | 7 | ABW02759 | | Abw02759 Angiogene |
| 8 | 26 | 100.0 | 7 | 7 | ABW02760 | | Abw02760 Angiogene |
| 9 | 26 | 100.0 | 9 | 8 | ADO39412 | | Ado39412 Contiguou |

| | | | | | | |
|----|----|-------|----|---|----------|--------------------|
| 10 | 26 | 100.0 | 11 | 2 | AAR25097 | Aar25097 bGRF prod |
| 11 | 26 | 100.0 | 12 | 5 | ABB80826 | Abb80826 Heparin b |
| 12 | 26 | 100.0 | 12 | 6 | ABR64030 | Abr64030 E. coli p |
| 13 | 26 | 100.0 | 12 | 7 | ADC44494 | Adc44494 Endotheli |
| 14 | 26 | 100.0 | 13 | 6 | ABU14452 | Abu14452 hFSH pept |
| 15 | 26 | 100.0 | 13 | 6 | ABU14453 | Abu14453 hFSH pept |
| 16 | 26 | 100.0 | 13 | 6 | ABU14451 | Abu14451 hFSH pept |
| 17 | 26 | 100.0 | 13 | 6 | ABU14449 | Abu14449 hFSH pept |
| 18 | 26 | 100.0 | 13 | 6 | ABU14448 | Abu14448 hFSH pept |
| 19 | 26 | 100.0 | 13 | 6 | ABU14450 | Abu14450 hFSH pept |
| 20 | 26 | 100.0 | 15 | 8 | ADS88902 | Ads88902 Peptide e |
| 21 | 26 | 100.0 | 17 | 6 | ADA74731 | Ada74731 Tryptical |
| 22 | 26 | 100.0 | 18 | 6 | ADA74730 | Ada74730 Tryptical |
| 23 | 26 | 100.0 | 19 | 2 | AAW16890 | Aaw16890 Helicobac |
| 24 | 26 | 100.0 | 19 | 6 | ADA74729 | Ada74729 Tryptical |
| 25 | 26 | 100.0 | 19 | 8 | ADN17105 | Adn17105 Second ge |
| 26 | 26 | 100.0 | 20 | 5 | AAU99411 | Aau99411 Human ECS |
| 27 | 26 | 100.0 | 20 | 8 | ADO80138 | Ado80138 Human mag |
| 28 | 26 | 100.0 | 20 | 8 | ADS51924 | Ads51924 tRNA (gua |
| 29 | 26 | 100.0 | 22 | 4 | AAO01366 | Aao01366 Human pol |
| 30 | 26 | 100.0 | 24 | 4 | AAO04347 | Aao04347 Human pol |
| 31 | 26 | 100.0 | 26 | 4 | AAO12271 | Aao12271 Human pol |
| 32 | 26 | 100.0 | 26 | 4 | AAO05706 | Aao05706 Human pol |
| 33 | 26 | 100.0 | 27 | 4 | AAO11884 | Aao11884 Human pol |
| 34 | 26 | 100.0 | 29 | 4 | AAO05109 | Aao05109 Human pol |
| 35 | 26 | 100.0 | 30 | 4 | AAB64810 | Aab64810 Human sec |
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| 38 | 26 | 100.0 | 30 | 4 | AAO04497 | Aao04497 Human pol |
| 39 | 26 | 100.0 | 31 | 4 | AAO05488 | Aao05488 Human pol |
| 40 | 26 | 100.0 | 31 | 4 | AAO10805 | Aao10805 Human pol |
| 41 | 26 | 100.0 | 31 | 4 | AAO13369 | Aao13369 Human pol |
| 42 | 26 | 100.0 | 31 | 4 | AAO05850 | Aao05850 Human pol |
| 43 | 26 | 100.0 | 32 | 4 | AAO11531 | Aao11531 Human pol |
| 44 | 26 | 100.0 | 32 | 4 | AAO11435 | Aao11435 Human pol |
| 45 | 26 | 100.0 | 32 | 4 | AAO05724 | Aao05724 Human pol |

ALIGNMENTS

RESULT 1

AAE26706

ID AAE26706 standard; peptide; 7 AA.

XX

AC AAE26706;

XX

DT 13-DEC-2002 (first entry)

XX

DE Matrix metalloprotease (MMP) substrate peptide #15.

XX

KW Angiogenesis; methionine aminopeptidase; MetAP-2; matrix metalloprotease; MMP; therapy; autoimmune disease; rheumatoid arthritis; ocular disorder; diabetic retinopathy; skin disorder; paediatric disorder; angiofibroma; psoriasis; cancer; sarcoma; carcinoma; hypertrophic scar.

XX

OS Unidentified.

XX
FH Key Location/Qualifiers
FT Modified-site 2
FT /note= "L-cyclohexylalanine"
FT Modified-site 4
FT /note= "L-2-aminobutyric acid"
FT Modified-site 5
FT /note= "Methyl cysteine; This residue is shown as Xaa in
FT the sequence shown as SEQ ID NO: 16 in the sequence
FT listing of the specification"
XX
PN WO200242295-A2.
XX
PD 30-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US046086.
XX
PR 01-NOV-2000; 2000US-00704251.
PR 05-OCT-2001; 2001US-00972772.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Olson GL, Self C, Lee L, Cook CM, Birktoft J;
XX
DR WPI; 2002-666821/71.
XX
PT New compounds comprising MetAP-2 inhibitory core e.g. 1-
PT oxaspiro(2.5)octane derivative, coupled to peptide which is matrix
PT metalloprotease substrate, useful for treating e.g. cancer or rheumatoid
PT arthritis, are angiogenesis inhibitors.
XX
PS Claim 47; Page 77; 98pp; English.
XX
CC The present invention relates to novel angiogenesis inhibitor compounds
CC comprising a methionine aminopeptidase (MetAP-2) inhibitory core (e.g. 1-
CC oxaspiro (2.5) octane derivative), coupled to a peptide which is a matrix
CC metalloprotease (MMP) substrate. Compounds of the invention are useful
CC for treating angiogenic diseases such as autoimmune diseases (e.g.
CC cancer, rheumatoid arthritis). They are also useful for treating ocular
CC disorders (e.g. diabetic retinopathy), disorders affecting the skin (e.g.
CC psoriasis), cancer (e.g. carcinoma, sarcoma), paediatric disorders (e.g.
CC angiofibroma) and disorders associated with surgery (e.g. hypertrophic
CC scars). The present sequence is MMP substrate peptide
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 26; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|||:|||
Db 1 PXAXCHA 7

RESULT 9

ADO39412
ID ADO39412 standard; peptide; 9 AA.
XX
AC ADO39412;
XX
DT 29-JUL-2004 (first entry)
XX
DE Contiguous capillary-related horse apomyoglobin peptide SeqID12.
XX
KW contiguous capillary; electrically conductive; pores; analyte;
KW electrolyte; electrospray source; electrophoresis separation;
KW electrical conductivity; macromolecular analyte detection sensitivity;
KW CE-ESI-MS device; horse.
XX
OS Equus caballus.
XX
PN WO2004038752-A2.
XX
PD 06-MAY-2004.
XX
PF 20-OCT-2003; 2003WO-US033200.
XX
PR 21-OCT-2002; 2002US-0420003P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Janini G, Isaaq HJ, Veenstra TD, Conrads TP, Wilkens KL;
XX
DR WPI; 2004-390013/36.
XX
PT Contiguous capillary useful for separating and electrospraying a fluid
PT e.g. peptides and proteins includes inlet end, spray tip and an
PT electrically conductive portion in proximity to the spray tip to block
PT the passage of analyte through it.
XX
PS Example; SEQ ID NO 12; 53pp; English.
XX
CC This invention relates to a novel contiguous capillary which includes an
CC inlet to supply fluid into the capillary, a spray tip for spraying fluid
CC out of the capillary and an electrically conductive portion in proximity
CC to the spray tip. The electrically conductive portion has pores of size
CC that block the passage of analyte and permits the passage of electrolyte
CC through it. The capillary is useful as an electrospray source in the
CC electrophoresis separation and electrospraying of fluid containing
CC analyte and electrolyte, for example peptides and proteins. The invention
CC minimises analyte loss while maintaining electrical conductivity and does
CC not require a sheathed opening or break in the capillary near the spray
CC tip. The capillaries are rugged, simple in design and effect an increase
CC in macromolecular analyte detection sensitivity of up to about 100-fold
CC in CE-ESI-MS devices. The invention enables the high-resolution
CC identification of analytes. The present sequence is that of a horse
CC apomyoglobin tryptic digest peptide which was used in the exemplification
CC of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 26; DB 8; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|:||
Db 1 PLAQSHA 7

RESULT 10

AAR25097

ID AAR25097 standard; protein; 11 AA.

XX

AC AAR25097;

XX

DT 25-MAR-2003 (revised)

DT 23-DEC-1992 (first entry)

XX

DE bGRF prodrug analogue 16.

XX

KW Bovine growth hormone releasing factor; dipeptidylpeptidase IV; DPP IV;

KW purification; medicament.

XX

OS Synthetic.

XX

PN WO9210576-A1.

XX

PD 25-JUN-1992.

XX

PF 12-DEC-1991; 91WO-US009152.

XX

PR 13-DEC-1990; 90US-00626727.

XX

PA (UPJO) UPJOHN CO.

XX

PI Kubiak TM, Sharma SK;

XX

DR WPI; 1992-234631/28.

XX

PT Non-naturally occurring fusion protein prodrug - is cleaved in=vivo by host di:peptidyl peptides IV to achieve sustained release, e.g. of growth hormone.

XX

PS Disclosure; Page 38; 55pp; English.

XX

CC The sequences given in AAR25082-109 and AAR25247-62 are N-terminally extended bovine growth hormone releasing factor (bGRF) prodrug analogues. CC The N-terminal extension is cleavable by dipeptidylpeptidase IV (DPP IV). CC Exposure of these bGRF prodrug analogues to DPP IV results in their conversion to desirable proteins. These prodrugs are converted to prodrugs using a patients endogenous DPP IV, thereby achieving sustained presence of the active drug in a patient and reducing the frequency of administration. These proteins are useful in purification methods were the N-terminal extension facilitates purification. They may also be used to prepare a medicament. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|:||
Db 3 PHAHHA 9

Search completed: February 11, 2005, 12:34:39
Job time : 165 secs

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OM protein - protein search, using sw model

Run on: February 11, 2005, 12:28:57 ; Search time 43 Seconds
(without alignments)
12.152 Million cell updates/sec

Title: US-10-001-945A-16

Perfect score: 26

Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 324380

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 26 | 100.0 | 7 | 4 | US-09-704-251-16 | Sequence 16, Appl |
| 2 | 26 | 100.0 | 7 | 4 | US-09-704-251-17 | Sequence 17, Appl |
| 3 | 26 | 100.0 | 11 | 1 | US-08-211-942-18 | Sequence 18, Appl |
| 4 | 26 | 100.0 | 11 | 5 | PCT-US91-09152-16 | Sequence 16, Appl |
| 5 | 26 | 100.0 | 19 | 1 | US-08-211-942-1 | Sequence 1, Appl |
| 6 | 26 | 100.0 | 26 | 3 | US-08-974-549A-57 | Sequence 57, Appl |
| 7 | 26 | 100.0 | 26 | 4 | US-08-912-951-57 | Sequence 57, Appl |
| 8 | 26 | 100.0 | 26 | 4 | US-09-402-181B-57 | Sequence 57, Appl |
| 9 | 26 | 100.0 | 26 | 4 | US-09-721-456-57 | Sequence 57, Appl |
| 10 | 26 | 100.0 | 37 | 1 | US-08-340-428B-7 | Sequence 7, Appl |
| 11 | 26 | 100.0 | 37 | 5 | PCT-US93-07306-7 | Sequence 7, Appl |
| 12 | 26 | 100.0 | 50 | 4 | US-09-621-976-5211 | Sequence 5211, Ap |
| 13 | 26 | 100.0 | 53 | 4 | US-09-621-976-6427 | Sequence 6427, Ap |
| 14 | 26 | 100.0 | 54 | 4 | US-09-513-999C-4567 | Sequence 4567, Ap |
| 15 | 26 | 100.0 | 59 | 4 | US-09-621-976-4384 | Sequence 4384, Ap |
| 16 | 26 | 100.0 | 60 | 3 | US-08-817-787-22 | Sequence 22, Appl |
| 17 | 26 | 100.0 | 60 | 4 | US-09-621-976-6245 | Sequence 6245, Ap |
| 18 | 26 | 100.0 | 60 | 4 | US-09-583-808-22 | Sequence 22, Appl |
| 19 | 26 | 100.0 | 61 | 4 | US-09-252-991A-29862 | Sequence 29862, A |
| 20 | 26 | 100.0 | 63 | 4 | US-09-621-976-7548 | Sequence 7548, Ap |
| 21 | 26 | 100.0 | 66 | 4 | US-09-270-767-40087 | Sequence 40087, A |
| 22 | 26 | 100.0 | 66 | 4 | US-09-270-767-55303 | Sequence 55303, A |
| 23 | 26 | 100.0 | 67 | 4 | US-09-252-991A-26524 | Sequence 26524, A |
| 24 | 26 | 100.0 | 67 | 4 | US-09-489-039A-12320 | Sequence 12320, A |
| 25 | 26 | 100.0 | 72 | 4 | US-09-621-976-4512 | Sequence 4512, Ap |
| 26 | 26 | 100.0 | 74 | 4 | US-09-270-767-60432 | Sequence 60432, A |
| 27 | 26 | 100.0 | 80 | 4 | US-09-205-258-939 | Sequence 939, App |
| 28 | 26 | 100.0 | 80 | 4 | US-09-621-976-5334 | Sequence 5334, Ap |
| 29 | 26 | 100.0 | 86 | 3 | US-09-134-001C-5488 | Sequence 5488, Ap |
| 30 | 26 | 100.0 | 88 | 4 | US-09-489-039A-8981 | Sequence 8981, Ap |
| 31 | 26 | 100.0 | 89 | 4 | US-09-621-976-6766 | Sequence 6766, Ap |
| 32 | 26 | 100.0 | 94 | 4 | US-09-328-352-5643 | Sequence 5643, Ap |
| 33 | 26 | 100.0 | 98 | 4 | US-09-543-681A-6937 | Sequence 6937, Ap |
| 34 | 23 | 88.5 | 11 | 3 | US-08-893-526A-16 | Sequence 16, Appl |
| 35 | 23 | 88.5 | 16 | 2 | US-08-528-057-12 | Sequence 12, Appl |
| 36 | 23 | 88.5 | 19 | 4 | US-09-132-769-12 | Sequence 12, Appl |
| 37 | 23 | 88.5 | 22 | 4 | US-09-464-152A-17 | Sequence 17, Appl |
| 38 | 23 | 88.5 | 29 | 4 | US-09-513-783A-132 | Sequence 132, App |
| 39 | 23 | 88.5 | 29 | 4 | US-09-430-656-132 | Sequence 132, App |
| 40 | 23 | 88.5 | 52 | 4 | US-09-270-767-36792 | Sequence 36792, A |
| 41 | 23 | 88.5 | 52 | 4 | US-09-270-767-52009 | Sequence 52009, A |
| 42 | 23 | 88.5 | 58 | 4 | US-09-270-767-37591 | Sequence 37591, A |
| 43 | 23 | 88.5 | 58 | 4 | US-09-270-767-52808 | Sequence 52808, A |
| 44 | 23 | 88.5 | 64 | 4 | US-09-270-767-40507 | Sequence 40507, A |
| 45 | 23 | 88.5 | 64 | 4 | US-09-270-767-55723 | Sequence 55723, A |

ALIGNMENTS

RESULT 1

US-09-704-251-16

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; Sequence 16, Application US/09704251
; Patent No. 6548477
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
```

; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106
; CURRENT APPLICATION NUMBER: US/09/704,251
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; OTHER INFORMATION: Xaa at position 2 represents L-cyclohexylalanine
; OTHER INFORMATION: Xaa at position 4 represents L-a-aminobutyryl
; OTHER INFORMATION: Xaa at position 5 represents methylated cysteine
US-09-704-251-16

Query Match 100.0%; Score 26; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|||
Db 1 PXAXXHA 7

RESULT 3
US-08-211-942-18
; Sequence 18, Application US/08211942
; Patent No. 5523287
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Thomas
; APPLICANT: Bialojan, Siegfried
; APPLICANT: Kroeger, Burkhard
; APPLICANT: Kuenast, Christoph
; TITLE OF INVENTION: No. 5523287el thrombin-inhibitory protein from
assassin
; TITLE OF INVENTION: bugs.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,942
; FILING DATE:

; CLASSIFICATION: 435
; CLASSIFICATION: C07K 13/00
; CLASSIFICATION: A61K 37/64
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP92/02450
; FILING DATE: 27-OCT-1992
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-211-942-18

Query Match 100.0%; Score 26; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 36;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|:||
Db 5 PCACCPHA 11

Search completed: February 11, 2005, 12:39:05
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 12:37:43 ; Search time 129 Seconds
(without alignments)
17.731 Million cell updates/sec

Title: US-10-001-945A-16

Perfect score: 26

Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 585885

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

| Result No. | Score | Query | | | | Description |
|---------------|-------|-------|--------|----|---------------------|-------------------|
| | | Match | Length | DB | ID | |
| 1 | 26 | 100.0 | 7 | 9 | US-09-972-772-16 | Sequence 16, Appl |
| 2 | 26 | 100.0 | 7 | 9 | US-09-972-772-17 | Sequence 17, Appl |
| 3 | 26 | 100.0 | 7 | 13 | US-10-001-945-16 | Sequence 16, Appl |
| 4 | 26 | 100.0 | 7 | 13 | US-10-001-945-17 | Sequence 17, Appl |
| 5 | 26 | 100.0 | 7 | 14 | US-10-138-935-16 | Sequence 16, Appl |
| 6 | 26 | 100.0 | 7 | 14 | US-10-138-935-17 | Sequence 17, Appl |
| 7 | 26 | 100.0 | 12 | 14 | US-10-286-457-222 | Sequence 222, App |
| 8 | 26 | 100.0 | 13 | 16 | US-10-203-969A-513 | Sequence 513, App |
| 9 | 26 | 100.0 | 13 | 16 | US-10-203-969A-514 | Sequence 514, App |
| 10 | 26 | 100.0 | 13 | 16 | US-10-203-969A-515 | Sequence 515, App |
| 11 | 26 | 100.0 | 13 | 16 | US-10-203-969A-516 | Sequence 516, App |
| 12 | 26 | 100.0 | 13 | 16 | US-10-203-969A-517 | Sequence 517, App |
| 13 | 26 | 100.0 | 13 | 16 | US-10-203-969A-518 | Sequence 518, App |
| 14 | 26 | 100.0 | 13 | 16 | US-10-642-553-361 | Sequence 361, App |
| 15 | 26 | 100.0 | 13 | 16 | US-10-642-553-362 | Sequence 362, App |
| 16 | 26 | 100.0 | 13 | 16 | US-10-642-553-363 | Sequence 363, App |
| 17 | 26 | 100.0 | 13 | 16 | US-10-642-553-364 | Sequence 364, App |
| 18 | 26 | 100.0 | 13 | 16 | US-10-642-553-365 | Sequence 365, App |
| 19 | 26 | 100.0 | 13 | 16 | US-10-642-553-366 | Sequence 366, App |
| 20 | 26 | 100.0 | 17 | 15 | US-10-289-009-14 | Sequence 14, Appl |
| 21 | 26 | 100.0 | 18 | 15 | US-10-289-009-13 | Sequence 13, Appl |
| 22 | 26 | 100.0 | 19 | 15 | US-10-289-009-12 | Sequence 12, Appl |
| 23 | 26 | 100.0 | 20 | 15 | US-10-430-685-80 | Sequence 80, Appl |
| 24 | 26 | 100.0 | 20 | 15 | US-10-416-090-2 | Sequence 2, Appl |
| 25 | 26 | 100.0 | 26 | 14 | US-10-044-692-57 | Sequence 57, Appl |
| 26 | 26 | 100.0 | 26 | 14 | US-10-044-539-57 | Sequence 57, Appl |
| 27 | 26 | 100.0 | 26 | 15 | US-10-325-810-57 | Sequence 57, Appl |
| 28 | 26 | 100.0 | 26 | 17 | US-10-877-146-57 | Sequence 57, Appl |
| 29 | 26 | 100.0 | 33 | 14 | US-10-029-386-31686 | Sequence 31686, A |

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|----|----|-------|----|----|----------------------|-------------------|
| 30 | 26 | 100.0 | 37 | 14 | US-10-164-279-51 | Sequence 51, Appl |
| 31 | 26 | 100.0 | 37 | 16 | US-10-437-963-178440 | Sequence 178440, |
| 32 | 26 | 100.0 | 38 | 11 | US-09-833-245-614 | Sequence 614, App |
| 33 | 26 | 100.0 | 38 | 15 | US-10-424-599-265177 | Sequence 265177, |
| 34 | 26 | 100.0 | 40 | 9 | US-09-764-869-880 | Sequence 880, App |
| 35 | 26 | 100.0 | 40 | 14 | US-10-091-504-880 | Sequence 880, App |
| 36 | 26 | 100.0 | 40 | 15 | US-10-227-577-880 | Sequence 880, App |
| 37 | 26 | 100.0 | 42 | 15 | US-10-424-599-211724 | Sequence 211724, |
| 38 | 26 | 100.0 | 43 | 16 | US-10-437-963-133265 | Sequence 133265, |
| 39 | 26 | 100.0 | 45 | 16 | US-10-475-446-28 | Sequence 28, Appl |
| 40 | 26 | 100.0 | 46 | 9 | US-09-764-869-854 | Sequence 854, App |
| 41 | 26 | 100.0 | 46 | 14 | US-10-091-504-854 | Sequence 854, App |
| 42 | 26 | 100.0 | 46 | 15 | US-10-227-577-854 | Sequence 854, App |
| 43 | 26 | 100.0 | 47 | 9 | US-09-864-761-42772 | Sequence 42772, A |
| 44 | 26 | 100.0 | 48 | 14 | US-10-144-929-168 | Sequence 168, App |
| 45 | 26 | 100.0 | 48 | 14 | US-10-029-386-28596 | Sequence 28596, A |

ALIGNMENTS

RESULT 1

US-09-972-772-16
; Sequence 16, Application US/09972772
; Publication No. US20020193298A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106CP
; CURRENT APPLICATION NUMBER: US/09/972,772
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; NAME/KEY: VARIANT
; LOCATION: 2
; OTHER INFORMATION: Xaa at position 2 represents L-cyclohexylalanine
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 represents L-a-aminobutyryl
; NAME/KEY: VARIANT
; LOCATION: 5
; OTHER INFORMATION: Xaa at position 5 represents methylated cysteine
US-09-972-772-16

Query Match 100.0%; Score 26; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|||
Db 1 PXAXXHA 7

RESULT 8
US-10-203-969A-513
; Sequence 513, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hFSH derived
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
US-10-203-969A-513

Query Match 100.0%; Score 26; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|:||
Db 6 PGAAHHA 12

Search completed: February 11, 2005, 12:49:59
Job time : 130 secs

OM protein - protein search, using sw model

Run on: February 11, 2005, 12:28:27 ; Search time 38 Seconds
(without alignments)
17.724 Million cell updates/sec

Title: US-10-001-945A-16

Perfect score: 26

Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 37678

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | | Description |
|--------|-------|-------|--------|----|--------|--------------------|
| No. | Score | Match | Length | DB | ID | |
| 1 | 26 | 100.0 | 55 | 2 | C82705 | hypothetical prote |
| 2 | 26 | 100.0 | 68 | 2 | I38590 | hypothetical prote |
| 3 | 26 | 100.0 | 80 | 2 | F82684 | hypothetical prote |
| 4 | 26 | 100.0 | 82 | 2 | T04476 | acclimation protei |
| 5 | 26 | 100.0 | 84 | 2 | AH2724 | hypothetical prote |
| 6 | 26 | 100.0 | 84 | 2 | D97506 | hypothetical prote |
| 7 | 26 | 100.0 | 93 | 2 | S14020 | hypothetical prote |
| 8 | 23 | 88.5 | 51 | 2 | T08488 | hypothetical prote |
| 9 | 23 | 88.5 | 51 | 2 | T07563 | hypothetical prote |
| 10 | 23 | 88.5 | 52 | 2 | C84395 | hypothetical prote |
| 11 | 23 | 88.5 | 57 | 2 | AF1381 | hypothetical prote |
| 12 | 23 | 88.5 | 62 | 2 | S73032 | hypothetical prote |
| 13 | 23 | 88.5 | 64 | 2 | E87083 | 50S ribosomal prot |
| 14 | 23 | 88.5 | 64 | 2 | E70619 | probable ribosomal |
| 15 | 23 | 88.5 | 69 | 1 | B35537 | cytochrome-c oxida |
| 16 | 23 | 88.5 | 69 | 1 | OSHU8 | cytochrome-c oxida |
| 17 | 23 | 88.5 | 69 | 2 | S71929 | cytochrome-c oxida |
| 18 | 23 | 88.5 | 82 | 1 | CCPS5S | cytochrome c551 [v |

| | | | | | | |
|----|----|------|----|---|--------|--------------------|
| 19 | 23 | 88.5 | 85 | 2 | C82706 | hypothetical prote |
| 20 | 23 | 88.5 | 90 | 2 | I38889 | transmembrane prot |
| 21 | 23 | 88.5 | 92 | 2 | B75602 | hypothetical prote |
| 22 | 23 | 88.5 | 93 | 2 | S14314 | neutrophil cationi |
| 23 | 23 | 88.5 | 93 | 2 | S21169 | neutrophil cationi |
| 24 | 23 | 88.5 | 95 | 2 | AG0505 | probable membrane |
| 25 | 23 | 88.5 | 95 | 2 | D83360 | hypothetical prote |
| 26 | 22 | 84.6 | 12 | 2 | S65730 | hemoglobin, extrac |
| 27 | 22 | 84.6 | 15 | 2 | S36893 | ribosomal protein |
| 28 | 22 | 84.6 | 20 | 2 | S72501 | protein kinase C i |
| 29 | 22 | 84.6 | 20 | 2 | PH0110 | style glycoprotein |
| 30 | 22 | 84.6 | 21 | 2 | S46550 | actin-related prot |
| 31 | 22 | 84.6 | 23 | 2 | D34047 | stylar glycoprotei |
| 32 | 22 | 84.6 | 25 | 2 | A58647 | alphaA-conotoxin P |
| 33 | 22 | 84.6 | 34 | 2 | E82284 | hypothetical prote |
| 34 | 22 | 84.6 | 37 | 2 | S14101 | apolipoporphin III |
| 35 | 22 | 84.6 | 39 | 2 | D85649 | hypothetical prote |
| 36 | 22 | 84.6 | 41 | 2 | S06270 | T-cell receptor de |
| 37 | 22 | 84.6 | 42 | 2 | G90911 | hypothetical prote |
| 38 | 22 | 84.6 | 46 | 2 | A60495 | T-cell receptor be |
| 39 | 22 | 84.6 | 47 | 2 | E81833 | hypothetical prote |
| 40 | 22 | 84.6 | 49 | 2 | B24696 | tissue kallikrein |
| 41 | 22 | 84.6 | 49 | 2 | T37008 | hypothetical prote |
| 42 | 22 | 84.6 | 49 | 2 | B83712 | hypothetical prote |
| 43 | 22 | 84.6 | 51 | 2 | E81212 | 50S ribosomal prot |
| 44 | 22 | 84.6 | 53 | 2 | H84319 | hypothetical prote |
| 45 | 22 | 84.6 | 53 | 2 | H82738 | hypothetical prote |

ALIGNMENTS

RESULT 1

C82705

hypothetical protein XF1238 [imported] - *Xylella fastidiosa* (strain 9a5c)
C;Species: *Xylella fastidiosa*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82705
R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for
Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: C82705
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-55 <SIM>
A;Cross-references: UNIPROT:Q9PDZ0; GB:AE003958; GB:AE003849; NID:g9106217;
PIDN:AAF84048.1; GSPDB:GN00128; XFSC:XF1238
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.;
Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros,
M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.;
Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Colauto, N.B.;
Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.;

Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.; Gomes, S.L.; Gruber, A.; Ho, P.L.; Hoheisel, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.; Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado, J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.L.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento, A.L.T.O.; Netto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto, B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.; Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, H.E.

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza, A.P.; Terenzi, M.F.; Truffi, D.; Tsai, S.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zatz, M.; Meidanis, J.; Setubal, J.C.

A:Reference number: A59328

A:Contents: annotation

II. Genetics:

A: Cope: XE1238

Query Match 100.0%; Score 26; DB 2; Length 55;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conserved 3; Mismatches 2; Indels 2; Gaps 0

Qy 1 PXAXXHA 7
|:|:||
D 14 PDXHOMA 2

Search completed: February 11, 2005, 12:38:18
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd

QM protein = protein search using sw model

Run on: February 11, 2005, 12:16:47 ; Search time 167 Seconds
(without alignments)
21.464 Million cell updates/sec

Title: US-10-001-945A-16

Perfect score: 26

Sequence: 1 PXAXXXHA 7

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 259284

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | | | | Description |
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| | Score | Match | Length | DB ID | |
| 1 | 26 | 100.0 | 29 | 2 Q65HQ6 | Q65hq6 bacillus li |
| 2 | 26 | 100.0 | 46 | 2 Q7Z4A7 | Q7z4a7 homo sapien |
| 3 | 26 | 100.0 | 51 | 2 Q9XST0 | Q9xst0 canis famil |
| 4 | 26 | 100.0 | 53 | 2 Q8XY57 | Q8xy57 ralstonia s |
| 5 | 26 | 100.0 | 54 | 2 Q68IP5 | Q68ip5 conus marmo |
| 6 | 26 | 100.0 | 55 | 2 Q9PDZ0 | Q9pdz0 xylella fas |
| 7 | 26 | 100.0 | 59 | 2 Q62K88 | Q62k88 burkholderi |
| 8 | 26 | 100.0 | 59 | 2 Q7UUG5 | Q7uug5 rhodopirell |
| 9 | 26 | 100.0 | 62 | 2 Q6PN82 | Q6pn82 conus marmo |
| 10 | 26 | 100.0 | 64 | 2 Q6PN83 | Q6pn83 conus marmo |
| 11 | 26 | 100.0 | 66 | 2 Q6PN84 | Q6pn84 conus marmo |
| 12 | 26 | 100.0 | 66 | 2 Q8RYT9 | Q8ryt9 oryza sativ |
| 13 | 26 | 100.0 | 67 | 2 Q63F35 | Q63f35 bacillus ce |
| 14 | 26 | 100.0 | 69 | 2 Q51084 | Q51084 neisseria m |
| 15 | 26 | 100.0 | 73 | 2 Q6ZLG6 | Q6zlg6 oryza sativ |
| 16 | 26 | 100.0 | 73 | 2 Q8FNI9 | Q8fni9 corynebacte |
| 17 | 26 | 100.0 | 76 | 2 Q6K7I6 | Q6k7i6 oryza sativ |
| 18 | 26 | 100.0 | 78 | 2 Q6AFX8 | Q6afx8 leifsonia x |
| 19 | 26 | 100.0 | 80 | 2 Q9PDG2 | Q9pdg2 xylella fas |
| 20 | 26 | 100.0 | 81 | 2 Q84Z16 | Q84z16 oryza sativ |
| 21 | 26 | 100.0 | 82 | 2 Q40033 | Q40033 hordeum vul |
| 22 | 26 | 100.0 | 82 | 2 Q6SEH3 | Q6seh3 xenopus lae |
| 23 | 26 | 100.0 | 84 | 2 Q87MM4 | Q87mm4 vibrio para |
| 24 | 26 | 100.0 | 84 | 2 Q8UG39 | Q8ug39 agrobacteri |
| 25 | 26 | 100.0 | 85 | 2 Q8S520 | Q8s520 cucumis mel |
| 26 | 26 | 100.0 | 85 | 2 Q8NTQ4 | Q8ntq4 corynebacte |
| 27 | 26 | 100.0 | 86 | 2 Q71DC3 | Q71dc3 drosophila |
| 28 | 26 | 100.0 | 87 | 2 Q8W0D9 | Q8w0d9 oryza sativ |
| 29 | 26 | 100.0 | 87 | 2 Q9XGU9 | Q9xgu9 orobanche r |
| 30 | 26 | 100.0 | 87 | 2 Q84EQ2 | Q84eq2 wautersia o |
| 31 | 26 | 100.0 | 88 | 2 Q7UGH0 | Q7ugh0 rhodopirell |
| 32 | 26 | 100.0 | 88 | 2 Q7VZL6 | Q7vzl6 bordetella |
| 33 | 26 | 100.0 | 90 | 1 NPP3_DROME | Q9vv28 drosophila |

| | | | | | | |
|----|----|-------|----|---|--------|--------------------|
| 34 | 26 | 100.0 | 90 | 2 | Q9BGV8 | Q9bgv8 macaca fasc |
| 35 | 26 | 100.0 | 91 | 2 | Q6ILY2 | Q6ily2 drosophila |
| 36 | 26 | 100.0 | 93 | 2 | Q99198 | Q99198 chlamydomon |
| 37 | 26 | 100.0 | 93 | 2 | Q7UWB2 | Q7uwb2 rhodopirell |
| 38 | 26 | 100.0 | 93 | 2 | Q82GB4 | Q82gb4 streptomyce |
| 39 | 26 | 100.0 | 94 | 2 | Q6IIR6 | Q6iir6 drosophila |
| 40 | 26 | 100.0 | 94 | 2 | Q8XW71 | Q8xw71 ralstonia s |
| 41 | 26 | 100.0 | 95 | 2 | Q9P0F7 | Q9p0f7 homo sapien |
| 42 | 26 | 100.0 | 97 | 2 | Q6ASY5 | Q6asy5 oryza sativ |
| 43 | 26 | 100.0 | 97 | 2 | Q6ESH3 | Q6esh3 oryza sativ |
| 44 | 26 | 100.0 | 98 | 2 | Q6ABF7 | Q6abf7 propionibac |
| 45 | 26 | 100.0 | 99 | 2 | Q8WVH6 | Q8wvh6 homo sapien |

ALIGNMENTS

RESULT 1

Q65HQ6

ID Q65HQ6 PRELIMINARY; PRT; 29 AA.
AC Q65HQ6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BLi02534;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
DR EMBL; AE017333; AAU41408.1; -.
KW Hypothetical protein.
SQ SEQUENCE 29 AA; 3050 MW; DEE9A2AEE7D3304F CRC64;

Query Match 100.0%; Score 26; DB 2; Length 29;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
Db 8 PTAASHA 14

Search completed: February 11, 2005, 12:37:34
Job time : 170 secs

=> fil reg; d stat que 17
FILE 'REGISTRY' ENTERED AT 17:05:07 ON 14 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 13 FEB 2005 HIGHEST RN 830317-64-1
DICTIONARY FILE UPDATES: 13 FEB 2005 HIGHEST RN 830317-64-1

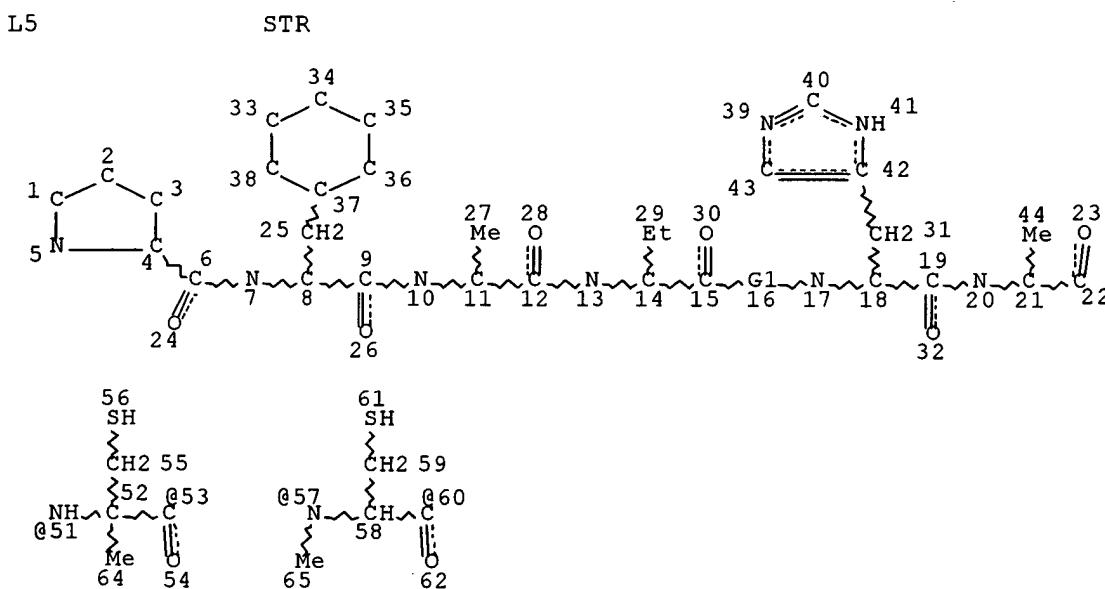
TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

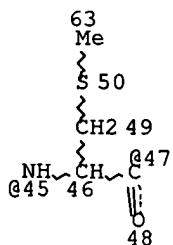
Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:

<http://www.cas.org/ONLINE/DBSS/registryss.html>



Page 1-A



Page 2-A
VAR G1=51-15 53-17/57-15 60-17/45-15 47-17

NODE ATTRIBUTES:
DEFAULT MLEVEL IS ATOM
DEFAULT ECLEVEL IS LIMITED

GRAPH ATTRIBUTES:
RING(S) ARE ISOLATED OR EMBEDDED
NUMBER OF NODES IS 65

STEREO ATTRIBUTES: NONE
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SEARCH TIME: 00.00.01

=> d sqide 17

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RN 478412-67-8 REGISTRY
CN L-Alanine, L-prolyl-3-cyclohexyl-L-alanyl-L-alanyl-(2S)-2-aminobutanoyl-S-methyl-L-cysteinyl-L-histidyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 14: PN: US20020193298 SEQID: 16 claimed protein

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 7

NTE modified (modifications unspecified)

| type | ----- location ----- | description |
|--------------|----------------------|-----------------|
| uncommon | Abu-4 | - |
| modification | Ala-2 | cyclohexyl<Chx> |
| modification | Cys-5 | methyl<Me> |

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given|US2002193298

|claimed

|SEQID 16

SEQ 1 PAAXCHA

MF C34 H55 N9 O8 S

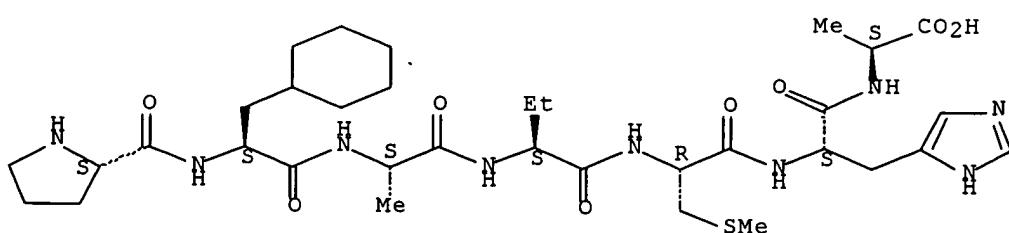
SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

DT.CA CAplus document type: Patent

RL.P Roles from patents: BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

Absolute stereochemistry.



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

2 REFERENCES IN FILE CA (1907 TO DATE)
2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> fil capl uspatf toxcenter; s 17
FILE 'CAPLUS' ENTERED AT 17:05:34 ON 14 FEB 2005
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L8 6 L7

=> dup rem 18
PROCESSING COMPLETED FOR L8
L9 2 DUP REM L8 (4 DUPLICATES REMOVED)
 ANSWERS '1-2' FROM FILE CAPLUS

=> d ibib ed abs hitrn 1-2; fil hom

L9 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2003:455053 CAPLUS Full-text
DOCUMENT NUMBER: 139:7179
TITLE: Preparation of compounds comprising a methionine
 aminopeptidase 2 (MetAP-2) inhibitory core coupled to
 a peptide for modulation of angiogenesis
INVENTOR(S): Olson, Gary L.; Self, Christopher; Lee, Lily; Cook,
 Charles Michael; Birktoft, Jens; Morgan, Barry;
 Arico-Muendel, Christopher C.
PATENT ASSIGNEE(S): Praecis Pharmaceuticals Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 48 pp., Cont.-in-part of U.S.
 Ser. No. 1,945.
 CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|------|----------|-----------------|----------|
| US 2003109671 | A1 | 20030612 | US 2002-138935 | 20020502 |
| US 6548477 | B1 | 20030415 | US 2000-704251 | 20001101 |
| US 2002193298 | A1 | 20021219 | US 2001-972772 | 20011005 |
| US 2002151493 | A1 | 20021017 | US 2001-1945 | 20011101 |
| WO 2003092608 | A2 | 20031113 | WO 2003-US13623 | 20030502 |
| WO 2003092608 | A3 | 20040115 | | |

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT,
TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1503749 A2 20050209 EP 2003-724378 20030502

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

PRIORITY APPLN. INFO.:

US 2000-704251 A2 20001101
US 2001-972772 A2 20011005
US 2001-1945 A2 20011101
US 2002-138935 A 20020502
WO 2003-US13623 W 20030502

OTHER SOURCE(S): MARPAT 139:7179

ED Entered STN: 13 Jun 2003

AB The invention provides angiogenesis inhibitor compds. A-W-CONR1-Xn-CR3R4-Z- P [A is a Met-AP-2 inhibitory core; W is O or NR2; R1, R2 are H or alkyl; X is alkylene or substituted alkylene; n is 0 or 1; R3, R4 are H, (un)substituted alkyl or (hetero)aryl; or CR3R4 is carbocyclic, heterocyclic, or alkylene; Z is CO or alkylene-CO and P is a peptide comprising 1 to about 100 amino acid residues attached at its amino terminus to Z or a group OR5 or NR6R7, where R5-R7 are H, alkyl, (un)substituted alkyl or azacycloalkyl or NR6R7 is (un)substituted heterocycl; or Z is O, NR6 (R8 = H or alkyl), alkylene-O, or alkylene-NR8 and P is H, alkyl or a peptide consisting of 1 to about 100 amino acid residues attached at its carboxy terminus to Z] comprising a MetAP-2 inhibitory core coupled to a peptide, as well as pharmaceutical compns. comprising the angiogenesis inhibitor compds. Thus, (3R,4S,5S,6R)-5-methoxy-4-[(2R, 3R)-2-methyl-3-(3-methylbut-2-enyl)oxiranyl]-1-oxaspiro[2.5]oct-6-ylcarbonyl-L-valine Me ester, prepared by acylation of L-valine Me ester hydrochloride, showed IC50 = 4.7 nM for inhibition of MetAP-2.

IT 478412-67-8P

RL: PNU (Preparation, unclassified); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

(preparation of peptide MetAP-2 inhibitory core derivs. for modulation of angiogenesis)

L9 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 2002:965105 CAPLUS Full-text

DOCUMENT NUMBER: 138:33374

TITLE: Therapeutic agents and methods of use thereof for the modulation of angiogenesis

INVENTOR(S): Olson, Gary L.; Self, Christopher; Lee, Lily; Cook, Charles Michael; Birktoft, Jens

PATENT ASSIGNEE(S): Praecis Pharmaceuticals Inc., USA

SOURCE: U.S. Pat. Appl. Publ., 38 pp., Cont.-in-part of U. S. Ser. No. 704,251.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 4

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|------|----------|-----------------|----------|
| US 2002193298 | A1 | 20021219 | US 2001-972772 | 20011005 |
| US 6548477 | B1 | 20030415 | US 2000-704251 | 20001101 |
| CA 2426703 | AA | 20020530 | CA 2001-2426703 | 20011101 |
| WO 2002042295 | A2 | 20020530 | WO 2001-US46086 | 20011101 |
| WO 2002042295 | A3 | 20030220 | | |

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,

| | | | |
|------------------------|---|-----------------|-------------|
| | PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, | | |
| | UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | |
| RW: | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, | | |
| | DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, | | |
| | BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | |
| AU 2002039479 | A5 20020603 | AU 2002-39479 | 20011101 |
| US 2002151493 | A1 20021017 | US 2001-1945 | 20011101 |
| EP 1330447 | A2 20030730 | EP 2001-987241 | 20011101 |
| R: | AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, | | |
| | IE, SI, LT, LV, FI, RO, MK, CY, AL, TR | | |
| JP 2004531466 | T2 20041014 | JP 2002-544429 | 20011101 |
| US 2003109671 | A1 20030612 | US 2002-138935 | 20020502 |
| NO 2003001978 | A 20030611 | NO 2003-1978 | 20030430 |
| PRIORITY APPLN. INFO.: | | US 2000-704251 | A2 20001101 |
| | | US 2001-972772 | A 20011005 |
| | | US 2001-1945 | A2 20011101 |
| | | WO 2001-US46086 | W 20011101 |

OTHER SOURCE(S): MARPAT 138:33374

ED Entered STN: 20 Dec 2002

AB The present invention provides angiogenesis inhibitor compds. comprising a MetAP-2 (methionine aminopeptidase-2)-inhibitory fumagillin core coupled to a peptide, as well as pharmaceutical compns. comprising the angiogenesis inhibitor compds. and a pharmaceutically acceptable carrier. The present invention also provides methods of treating an angiogenic disease, e.g., cancer, in a subject by administering to the subject a therapeutically effective amount of one or more of the angiogenesis inhibitor compds. of the invention.

IT 478412-67-8P

RL: PNU (Preparation, unclassified); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

(MetAP-2-inhibitory peptides for the modulation of angiogenesis)

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